

No new matter has been added with this amendment.

Claims 11-31 have been cancelled without prejudice. Applicants reserve the right to file a division and/or continuation on the cancelled subject matter.

Rejection under 35 U.S.C. § 102(b)

The Examiner has rejected Claims 5, 9, and 10 under 35 U.S.C. § 102 (b) as anticipated by WO96/08582. The Examiner states that the cited reference discloses *S. epidermidis* primers. This rejection, to the extent that it applies to the claims as amended is respectfully traversed.

To anticipate a claim under 35 U.S.C. § 102 (b), the reference must contain all of the elements of the claimed limitations. WO 96/08582 contains 4 primers that consist of no more than 25 to 30 nucleotides. Claims 9 and 10 as amended claim a probe or isolated nucleotide sequence that comprises at least 40 nucleotides of the SEQ ID NO:1835. Claim 5 also has been amended to obviate the alleged rejection. Thus WO 96/08582 does not anticipate the claimed invention.

The Examiner has rejected Claims 5, 9, and 10 under 35 U.S.C. § 102 (b) as anticipated by U.S. Patent No. 5,770,375 ('375 patent). The Examiner identifies Example 2 and 3 of the '375 patent as containing *S. epidermidis* primers which correlate to SEQ ID NO:5 – SEQ ID NO:8 of the '375 patent. The Applicants have provided the Examiner Exhibits A-D describing with sequence alignments between the claimed sequence SEQ ID NO:1835 and SEQ ID NO:5 – SEQ ID NO:8 disclosed in the Patent '375. As shown in Exhibits A-D detailing the alignments, the sequence overlaps do not exceed 20 bases. Moreover, the amended claims providing the number of nucleotide bases as 40 bases in claims 9 and 10 and the number the 10 amino acids of claim 5, overcome the alleged rejection under 35 U.S.C. § 102 (b).

Withdrawal of these rejections is respectfully requested.

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Conclusion

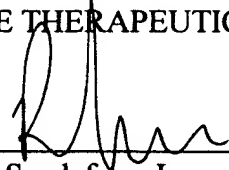
Reconsideration and withdrawal of the pending rejections are respectfully requested and a Notice of Allowance is earnestly solicited.

If the Examiner feels that a telephone conference would expedite prosecution of this application, he is invited to call the undersigned at 781-398-2300.

Any deficiency or overpayment for this reply should be charged or credited to Deposit Account No. 50-1040. One duplicate copy of this letter is enclosed.

Respectfully submitted,

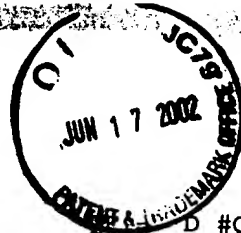
GENOME THERAPEUTICS CORPORATION

By 
Robert L. Spadafora, Jr.
Registration No 46,197
Telephone (781) 398-2300
Facsimile (781) 398-2607

Waltham, Massachusetts 02453
Dated:

4/3/02

SEQ ID NO:5 vs SEQ ID NO:1835



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Q = CGI_26caws20d648.seq
T = SEQ
A =
D = ID NO:1835
Identical Match = 282 Similar = 282 Total # Of Gaps = 41
Identity: Alignment = 54% Query = 11% Target = 54%
Similarity: Alignment = 54% Query = 11% Target = 54%
QS = 487 QE = 974 TS = 2 TE = 434
D #Q Symbols = 2362
D #T Symbols = 519

Q 487 AAAAAGTTGAAATTTTACAAGATAACGGA-AATGTTAAGAG-GAGA-AAGCTGATTGATT
A A ACTT T TTAC GA AA GGA AAT TA GAG AGA AAG A T ATT
T 2 AGATACTT----TGTTACTTGAAAAAGGAGAATAATATGAGTAAGACAAGAGCAGTTATT

Q 544 CACTTTAACTATGATAGAACATTATCAGTTATTG---CTGAAATAAAATCGAA--AAGC-
C C TA T TGAT A ATTA CA TAT G CT A ATA AT GAA AAGC
T 58 CCCGGTAGTTTTGATCCA--ATTA-CA--TATGGTCACTTAGATATCATTGAAAGAAGCG

Q 598 CCATCTGTACCTCAATTACCGCAACGTGATCTTGTTCAACAAGTTAAAGATTATCAAAAA
CC C G C T AT A C A GT TTGT A AA AAA A TA AAA
T 113 CCGACCG--CTTTGATGAAATCCATGT----TTGTGTACTAA--AAAATAGTAGTAAA--

Q 658 TATGGTGCTAATGCTATTTCAATATTAAGTATGAA--AAATACTTTGGCGGTAGTTTTG
GGTG AA G TTT A T C GA GAA A AC TTG G AG T
T 163 ---GGTG-GAACG---TTTGACT-----CAGAAGAACGCATGACGTTGATTGAAGAGT--

Q 716 AACGATTAAATCAGTTATCAAAGATAACATCGTTACCAGTTTTATGTAAAGAT--TTTAT
CG TTAAA CA TT C AA AT ACA A CA TTT ATG A G T TT AT
T 209 --CGGTTAAA-CATTTGCCTAATAT-ACAAGTGCATCATTTTAATGGATTGCTTGTGAT

Q 774 TATTGATAAAATTCAAATAGATGTTGCAAAACGAGCTGGTGCATCTATTATTTTA---TT
T TTG A TCAA TA G TGCAA GA C ATTATT A TT
T 265 TTTTGTGA----TCAAGTA---GGTGCAA--GA-----CAATTATTCGAGGTTT

Q 831 AATA---GTAAAT-ATTTTAAGTGATGACCAATTAAAAGAATTGTATTCATATGCAACAA
AA A GTAA T A TTT A T ATGA C A GA T TA T TATG AACAA
T 306 AAGAGCTGTAAGTGACTTTGAAT-ATGAAC-----TACGACT--TACTTCTATG-AACAA

Q 887 ACCATAATTTAGAAGCTCTAGTAGAAGTTCATACAAT-TAGAGAAGTTGA-ACGTGCACA
A AA TTA A TAGTA A TT A ACAAT TA A A TGA A GTGCA A
T 357 A----AAGTTAAA-----TAGTA-ATATTGAAACAATGTACATGA--TGACAAGTGCAA

Q 945 CCA---AATTAACCCTAAAATTATTGGTGTAA
C A A TTA T AA TAT TGTAA
T 405 CTATTCATTTATAAGTTCAAGTAT---TGTTAA

EXHIBIT A

SEQ ID NO:6 vs SEQ ID NO:1835



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RANK 1 Score = 322.00 P_Score = -1.0e+00

Q = CGI_26cbws24d66a.seq

QF = D #Q Symbols = 8654

T = SEQ

TF = D #T Symbols = 519

A =

D = ID NO:1835

Identical Match = 234 Similar = 234 Total # Of Gaps = 30

Identity: Alignment = 55% Query = 2% Target = 45%

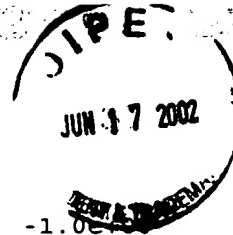
Similarity: Alignment = 55% Query = 2% Target = 45%

QS = 2974 QE = 3380 TS = 62 TE = 429

Q 2974 GTATTTTGGAGTTCCTCATATAAATGATCTTTTTCATA--ATTGTAATATTCTAACACTG
GTA TTT GA TCC TA A ATG TC TT ATA ATTG AA A A C C
T 62 GTAGTTTTGA--TCCAATTACATATGGTCACTTAGATATCATTGAAAGA----AGCGC-C
Q 3032 GAGTGTTTTTAGATACTTTGCTATGATTTTTTACTAAAAGTTTTTGGAGTTGTCCTAAAG
GA G TTT A A T C ATG TT T TACTAAAA A T GT TAAAG
T 115 GACCGCTTTGATGAAAT---CCATGTTTGTGTACTAAAA-----AATAGTAGTAAAG
Q 3092 TGGGAGTGTAGTAGAAAATATAGCTGTTAAGAGGGGCTTGTATACCAGTTG-TTGAAAGG
GT GAA T T CT AAGA GC TG AC GTTG TTGAA G
T 164 -----GTGGAACGTTTGACTCAGAAGA-ACGCATG---AC--GTTGATTGAA--G
Q 3151 AGTAATTTGGGC-TTTG-CTTTTATA-GTTTTTATATTTTAAATATCTTCTGTTTTAGAA
AGT TT C TTTG CT TATA T AT TTTTAAT T TG TT
T 206 AGTCGGTTAAACATTTGCCTAATATACAAGTGCATCATTTTAATGGAT--TGCTT-----
Q 3208 GTTAATTT---AGAGAAAGTA-ATGTAATAAACTA--CAAGTTGTGAGA-ATGAAAAT
GTT ATTT GA AAGTA TG AA A AA TA C AG T T AGA TG AA T
T 259 GTTGATTTTTGTGATCAAGTAGGTGCAAAGACAATTATTTCGAGGTTTAAGAGCTGTAAGT
Q 3261 GAATAGTAATGAAGAAATAACGA-TGCGTTGCTTGGTCATGGATGTTACCTCATAATAT
GA T AAT A GAA T ACGA T TT TG CA A GTT A ATA TA
T 319 GACTTTGAAT-ATGAACT-ACGACTTACTTCTATGAACA-AAAAGTTAA----ATAGTAA
Q 3320 TATTGTGAGGTTATTATACACTATTATTTTAAATGAAATATATTAATTT-TAAAT--AAG
TATTG A A T TAC AT AT AA TG AA TATT ATTT TAA T AAG
T 372 TATTGAAA---CAATGTAC---ATGATGACAAGTGCAAACCTATTTCATTTATAAGTTCAAG
Q 3377 CATT
ATT
T 426 TATT

EXHIBIT B

SEQ ID NO:7 vs SEQ ID NO:1835



RANK 1 Score = 345.00 P_Score = -1.00

Q = CGI_26ccws22157d.seq

QF = D #Q Symbols = 5024

T = SEQ

TF = D #T Symbols = 519

A =

D = ID NO:1835

Identical Match = 156 Similar = 156 Total # Of Gaps = 17

Identity: Alignment = 56% Query = 3% Target = 30%

Similarity: Alignment = 56% Query = 3% Target = 30%

QS = 3068 QE = 3318 TS = 225 TE = 474

Q 3068 TGATATAGAA---CCCTTTTGTGATGTCTTATGATAAATTAATAGACTTTTGTAAAAAAC
T ATATA AA C TTTT ATG GAT TT T GA TTTTGT A AA
T 225 TAATATACAAGTGCATCATTTTAAATG-----GATTGCTT-GTTGATTTTGTGATCAAG

Q 3124 AAGCT--ATAGACAAAGTTGTTGTTGCAGGTGATATTATGAGTTATCA-TCACGAAGAAT
AG T A AGACAA TT TT AGGT TTA GAG T T A T AC GAAT
T 278 TAGGTGCAAAGACAA-----TTATTCGAGGT---TTAAGAGCTGTAAGTGACTTTGAAT

Q 3181 ATG----ACATTTTACATCAAAGGA-AACGATTTAAACAAGCTAATATTCAAGTAATAT-
ATG AC TTAC TC A G A AA A TTAAA A TAATATT AA AAT T
T 329 ATGAACTACGACTTACTTCTATGAACAAAAGTTAAATA--GTAATATTGAAACAATGTA

Q 3235 CAT-----TAAGAGCAAATCATT-ATTT-TAACCCCGCAAAACACATAATAAACAAGGG
CAT AAG GCAAA ATT ATTT TAA G AA T TAAA AAG
T 387 CATGATGACAAGTGCAAATTCATTTATAA-----GTTCAAGTATTGTTAAAGAAGTA

Q 3288 GAACCATATAAAG-----TATTTACCAGTTTTTATA
G CATAT AAG ATTT CA TTTT TA
T 442 GCTGCATATCAAGCGGACATTT--CACCTTTTGTA

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EXHIBIT C

SEQ ID NO:8 vs SEQ ID NO:1835



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RANK 1 Score = 288.00 P_Score = -1.0e+00

Q = CGI_26cdws332f0b.seq

QF = D #Q Symbols = 3287

T = SEQ

TF = D #T Symbols = 519

A =

D = ID NO:1835

Identical Match = 233 Similar = 233 Total # Of Gaps = 29

Identity: Alignment = 55% Query = 7% Target = 44%

Similarity: Alignment = 55% Query = 7% Target = 44%

QS = 1617 QE = 2014 TS = 134 TE = 519

Q 1617 ATGTCAGGCTATCGAAATTATCAGTATTTAA-GTGA----CTGGCAAAGAGAAC-CAT
ATGT G TA C AAA AT AGTA T AA GTGA TG C A AGAAC CAT
T 134 ATGTTTGTGTA-CTAAAAAAT-AGTAGTAAAGGTGGAACGTTTGACTCAGAAGAACGCAT

Q 1671 -TCTTTGGTGTTCATTTGTCGTGGTAATTTTTGC----TATAGGTGGCGTACCTCCTTT
C TTG TTG A GTCG AA TTTGC TATA GT C TC TTT
T 192 GACGTTG--ATTG-AAGAGTCGGTTAAACATTTGCCTAATATA---CAAGTGCATCATTT

Q 1726 TAGTGGCTTTCCGGGTAAAGTCTTAATATTCCA--AGGGGCTATTACAAATGGTAATTAT
TA TGG TT C G T A T TT T TC A AGG GC A ACAA T ATT
T 246 TAATGGATTGCTTGTGA--TTTTTGTGATCAAGTAGGTGCAAAGACAA----TTATTGC

Q 1784 ATTGGTTTAGCACTTATGATTGTGACAAGTTTAATTGCTATGTA-TAGTCTTTTAGAGT
A GGTTTA A T T A GTGAC TTT A TATG A TA C TTA
T 300 A--GGTTTAAGAGCTGTAA--GTGAC---TTTGA---ATATGA ACTA--CGACTTACTTC

Q 1843 GATGTTTATAATGTATTTTGGTGATGCTGACGGAGAACAA-GTACAATTTAGACCA---C
ATG A AA GT T GT AT TGA AACAA GTAC AT GAC A C
T 348 TATGAACAAAAAGTTAAATAGTAATATTGA-----AACAAATGTAC-ATGATGACAAGTGC

Q 1899 TACCTATTTATCGTAAAGGTTTACTTAGTGTTTTAGTTGTAGTGGTATTAGCGA-TGGGT
A CTATT AT TA A GTT A TA TGTT AG GTAG G A TA C A GG
T 402 AAAC TATTCAT-TTATAAGTTCAAGTATTGTTAAAGAAGTAGCTGCA-TATCAAGCGGAC

Q 1958 ATTGCAGCCCCTGTTGT----TCTGAAAGTAACAGAGGATGCAACA--AATCTTAATATG
ATT CA CCT TTGT CT A A AGAG AT AA A AA TTAAT T
T 460 ATTTCA---CCTTTTGTACCACCTCATGTCGAAAGAGCATTAAAAAAGAAATTTAATGTT

Q 2012 AAA
AA
T 517 TAA

EXHIBIT D



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CLAIMS

5 1. (Amended) An isolated nucleic acid comprising a nucleotide sequence
encoding an *S. epidermidis* polypeptide ~~selected from the group consisting of~~ SEQ ID
NO: 3773 ~~SEQ ID NO: 7544~~ 5607.

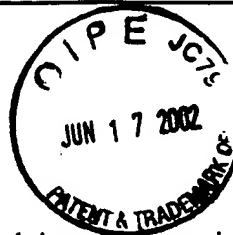
10 5. (Amended) An isolated nucleic acid comprising a nucleotide sequence
encoding an *S. epidermidis* polypeptide or a fragment of at least ten amino acid residues
~~thereof, said nucleic acid selected from the group consisting of~~ SEQ ID NO: 1835 ~~SEQ~~
~~ID NO: 3772~~.

15 9. (Amended) A probe comprising a nucleotide sequence consisting of at least
fortyeight contiguous nucleotides of a nucleotide sequence ~~selected from the group~~
~~consisting of~~ SEQ ID NO: ~~1~~ ~~SEQ ID NO: 3772~~ 1835.

20 10. (Amended) An isolated nucleic acid comprising a nucleotide sequence of at
least ~~eight~~ forty nucleotides in length, wherein the sequence is hybridizable to a nucleic
acid having a nucleotide sequence ~~selected from the group consisting of~~ SEQ ID NO: ~~1~~
~~SEQ ID NO: 3772~~ 1835.

Clean Version Claims

CLAIMS



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- 5 1. (Amended) An isolated nucleic acid comprising a nucleotide sequence
encoding an *S. epidermidis* polypeptide of SEQ ID NO:5607.
5. (Amended) An isolated nucleic acid comprising a nucleotide sequence
encoding an *S. epidermidis* polypeptide or a fragment of at least ten amino acid residues ,
10 said nucleic acid of SEQ ID NO:1835.
9. (Amended) A probe comprising a nucleotide sequence consisting of at least
forty contiguous nucleotides of a nucleotide sequence of SEQ ID NO:1835.
- 15 10. (Amended) An isolated nucleic acid comprising a nucleotide sequence of at
least forty nucleotides in length, wherein the sequence is hybridizable to a nucleic acid
having a nucleotide sequence of SEQ ID NO: 1835.